RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/627,952Source: IFwoDate Processed by STIC: 07/26/2005

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 07/26/2005

PATENT APPLICATION: US/10/627,952

TIME: 09:49:42

Input Set : N:\Crf3\RULE60\10627952.raw
Output Set: N:\CRF4\07262005\J627952.raw

SEQUENCE LISTING

| SEQUENCE LISTING | | | |
|------------------|----------------------------|--|--|
| 1 | 1 (1) GENERAL INFORMATION: | | |
| 2 | (i) | APPLICANT: Dong, Jin-Tang; Barrett, | |
| 3 | | J. Carl; Lamb, Patricia W.; Isaacs, John T. | |
| 4 | (ii) | TITLE OF INVENTION: DIAGNOSTIC METHODS AND | |
| 5 | | GENE THERAPY USING REAGENTS DERIVED FROM THE | |
| 6 | | HUMAN METASTASIS SUPPRESSOR GENE KAI1 | |
| 7 | (iii) | NUMBER OF SEQUENCES: 20 | |
| 8 | | CORRESPONDENCE ADDRESS: | |
| 9 | ,, | (A) ADDRESSEE: MORGAN & FINNEGAN, L.L.P. | |
| 10 | | (B) STREET: 345 PARK AVENUE | |
| 11 | | (C) CITY: NEW YORK | |
| 12 | | (D) STATE: NEW YORK | |
| 13 | | (E) COUNTRY: USA | |
| 14 | | (F) ZIP: 10154 | |
| 15 | (v) | COMPUTER READABLE FORM: | |
| 16 | (, | (A) MEDIUM TYPE: FLOPPY DISK | |
| 17 | | (B) COMPUTER: IBM PC COMPATIBLE | |
| 18 | | (C) OPERATING SYSTEM: PC-DOS/MS-DOS | |
| 19 | | (D) SOFTWARE: MICROSOFT WORD 97 | |
| 20 | (vi) | CURRENT APPLICATION DATA: | |
| C> 21 | , , | (A) APPLICATION NUMBER: US/10/627,952 | |
| C> 22 | | (B) FILING DATE: 24-Jul-2003 | |
| 23 | (vii) | PRIOR APPLICATION DATA: | |
| W> 24 | | (A) APPLICATION NUMBER: US/09/795,380 | |
| 25 | | (B) FILING DATE: 27-Feb-2001 | |
| W> 26 | | (A) APPLICATION NUMBER: 09/232,507 | |
| 27 | | (B) FILING DATE: | |
| 28 | (viii) | ATTORNEY/AGENT INFORMATION: | |
| 29 | | (A) NAME: RICHARD W. BORK | |
| 30 | | (B) REGISTRATION NUMBER: 36,459 | |
| 31 | | (C) REFERENCE/DOCKET NUMBER: 2026-4172US1 | |
| 32 | (ix) | TELECOMMUNICATION INFORMATION: | |
| 33 | | (A) TELEPHONE: (212) 758-4800 | |
| 34 | | (B) TELEFAX: (212) 751-6849 | |
| 35 | | (C) TELEX: 421792 | |
| 36 | (2) INFO | RMATION FOR SEQ ID NO: 1: | |
| 37 | (i) | SEQUENCE CHARACTERISTICS: | |
| 38 | | (A) LENGTH: 20 base pairs | |
| 39 | | (B) TYPE: nucleic acid | |
| 40 | | (C) STRANDEDNESS: single | |
| 41 | | (D) TOPOLOGY: linear | |
| 42 | (xi) | SEQUENCE DESCRIPTION: SEQ ID NO: 1: | |

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| 43 | | AGAAGATCAA GTTGAAGAGG | 20 |
|----|-----|--|-----|
| 45 | (2) | INFORMATION FOR SEQ ID NO: 2: | |
| 46 | ν-, | (i) SEQUENCE CHARACTERISTICS: | |
| 47 | | (A) LENGTH: 20 base pairs | |
| 48 | | (B) TYPE: nucleic acid | |
| 49 | | (C) STRANDEDNESS: single | |
| 50 | | (D) TOPOLOGY: linear | |
| 51 | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: | |
| 52 | | GGGACCTCAT TTCCTAGCTG | 20 |
| 54 | (2) | · · · · · · · · · · · · · · · · · · · | |
| 55 | (2) | (i) SEQUENCE CHARACTERISTICS: | |
| 56 | | (A) LENGTH: 19 base pairs | |
| 57 | | (B) TYPE: nucleic acid | |
| 58 | | (C) STRANDEDNESS: single | |
| | | (D) TOPOLOGY: linear | |
| 59 | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3: | |
| 60 | | | 19 |
| 61 | (0) | ATGAAACTGC TCTTGTCGG | 19 |
| 63 | (2) | ~ | |
| 64 | | (i) SEQUENCE CHARACTERISTICS: | |
| 65 | | (A) LENGTH: 20 base pairs | |
| 66 | | (B) TYPE: nucleic acid | |
| 67 | | (C) STRANDEDNESS: single | |
| 68 | | (D) TOPOLOGY: linear | |
| 69 | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4: | 20 |
| 70 | | TCAGCTCTTG GCTCCCCATT | 20 |
| 72 | (2) | ~ | |
| 73 | | (i) SEQUENCE CHARACTERISTICS: | |
| 74 | | (A) LENGTH: 21 base pairs | |
| 75 | | (B) TYPE: nucleic acid | |
| 76 | | (C) STRANDEDNESS: single | |
| 77 | | (D) TOPOLOGY: linear | |
| 78 | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5: | 0.1 |
| 79 | | TGGGCACGGG TTTCAGGAAA T | 21 |
| 81 | (2) | | |
| 82 | | (i) SEQUENCE CHARACTERISTICS: | |
| 83 | | (A) LENGTH: 20 base pairs | |
| 84 | | (B) TYPE: nucleic acid | |
| 85 | | (C) STRANDEDNESS: single | |
| 86 | | (D) TOPOLOGY: linear | |
| 87 | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6: | |
| 88 | | TGCAGAGAGC CCCAAATGCA | 20 |
| 90 | (2) | ~ | |
| 91 | | (i) SEQUENCE CHARACTERISTICS: | |
| 92 | | (A) LENGTH: 20 base pairs | |
| 93 | | (B) TYPE: nucleic acid | |
| 94 | | (C) STRANDEDNESS: single | |
| 95 | | (D) TOPOLOGY: linear | |
| 96 | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: | |
| 97 | | AGGGTGAGCC GTGAGCACAA | 20 |
| | | | |

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| 99 (2) INFORMATION FOR SEQ ID NO: 8: | |
|--|-----|
| 100 (i) SEQUENCE CHARACTERISTICS: | |
| 101 (A) LENGTH: 20 base pairs | |
| 102 (B) TYPE: nucleic acid | |
| 103 (C) STRANDEDNESS: single | |
| 104 (D) TOPOLOGY: linear | |
| 105 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8: | |
| 106 TGCTGAGAGT ACCCAGATGC | 20 |
| 108 (2) INFORMATION FOR SEQ ID NO: 9: | |
| 108 (2) INFORMATION FOR BEG 15 NO. 3. 109 (i) SEQUENCE CHARACTERISTICS: | |
| | |
| 110 (A) LENGTH: 19 base pairs 111 (B) TYPE: nucleic acid | |
| | |
| | |
| | |
| 114 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9: | 19 |
| 115 GATGGCCACA CCCACGCCC | 13 |
| 117 (2) INFORMATION FOR SEQ ID NO: 10: | |
| 118 (i) SEQUENCE CHARACTERISTICS: | |
| 119 (A) LENGTH: 20 base pairs | |
| 120 (B) TYPE: nucleic acid | |
| 121 (C) STRANDEDNESS: single | |
| 122 (D) TOPOLOGY: linear | |
| 123 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10: | 2.0 |
| 124 TGCATGGAGA AGGTGCAGGC | 20 |
| 126 (2) INFORMATION FOR SEQ ID NO: 11: | |
| 127 (i) SEQUENCE CHARACTERISTICS: | |
| 128 (A) LENGTH: 21 base pairs | |
| 129 (B) TYPE: nucleic acid | |
| 130 (C) STRANDEDNESS: single | |
| 131 (D) TOPOLOGY: linear | |
| 132 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11: | |
| 133 CCTCTTGCCC ACCCTGACTGA | 21 |
| 135 (2) INFORMATION FOR SEQ ID NO: 12: | |
| 136 (i) SEQUENCE CHARACTERISTICS: | |
| 137 (A) LENGTH: 20 base pairs | |
| 138 (B) TYPE: nucleic acid | |
| 139 (C) STRANDEDNESS: single | |
| 140 (D) TOPOLOGY: linear | |
| 141 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12: | |
| 142 TTCACACCAT TCTCCTGCCT | 20 |
| 144 (2) INFORMATION FOR SEQ ID NO: 13: | |
| 145 (i) SEQUENCE CHARACTERISTICS: | |
| 146 (A) LENGTH: 21 base pairs | |
| 147 (B) TYPE: nucleic acid | |
| 148 (C) STRANDEDNESS: single | |
| 149 (D) TOPOLOGY: linear | |
| 150 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13: | |
| 151 AGTCCTCCCT GCTGCTGTGT G | 21 |
| 153 (2) INFORMATION FOR SEQ ID NO: 14: | |
| | |

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| 154 | | (i) SEQUENCE CHARACTERISTICS: | |
|-----|---------------------|---|-----|
| 155 | | (A) LENGTH: 21 base pairs | |
| 156 | | (B) TYPE: nucleic acid | |
| 157 | | (C) STRANDEDNESS: single | |
| 158 | | (D) TOPOLOGY: linear | |
| 159 | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14: | |
| 160 | | TCAGTCAGGG TGGGCAAGAG G | 21 |
| 162 | (2) | INFORMATION FOR SEQ ID NO: 15: | |
| 163 | | (i) SEQUENCE CHARACTERISTICS: | |
| 164 | | (A) LENGTH: 22 base pairs | |
| 165 | | (B) TYPE: nucleic acid | |
| 166 | | (C) STRANDEDNESS: single | |
| 167 | | (D) TOPOLOGY: linear | |
| 168 | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15: | |
| 169 | | GAGGAGCACC CCGTGCTGCT GA22 | |
| | (2) | INFORMATION FOR SEQ ID NO: 16: | |
| 172 | | (i) SEQUENCE CHARACTERISTICS: | |
| 173 | | (A) LENGTH: 33 base pairs | |
| 174 | | (B) TYPE: nucleic acid | |
| 175 | | (C) STRANDEDNESS: single | |
| 176 | | (D) TOPOLOGY: linear | |
| 177 | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16: | |
| 178 | | CTAGAAGCAT TTGCGGTGGA CGATGGAGGG GCC33 | |
| | (2) | INFORMATION FOR SEQ ID NO: 17: | |
| 181 | \ - <i>\</i> | (i) SEQUENCE CHARACTERISTICS: | |
| 182 | | (A) LENGTH: 24 base pairs | |
| 183 | | (B) TYPE: nucleic acid | |
| 184 | | (C) STRANDEDNESS: single | |
| 185 | | (D) TOPOLOGY: linear | |
| 186 | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17: | |
| 187 | | TTGTAACCAA CTGGGACGAT ATGG24 | |
| | (2) | INFORMATION FOR SEQ ID NO: 18: | |
| 190 | (-, | (i) SEQUENCE CHARACTERISTICS: | |
| 191 | | (A) LENGTH: 23 base pairs | |
| 192 | | (B) TYPE: nucleic acid | |
| 193 | | (C) STRANDEDNESS: single | |
| 194 | | (D) TOPOLOGY: linear | |
| 195 | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18: | |
| 196 | | GTCTTGATCT TCATGGTGCT AGG23 | |
| 198 | (2) | INFORMATION FOR SEQ ID NO: 19: | |
| 199 | (2) | (i) SEQUENCE CHARACTERISTICS: | |
| 200 | | (A) LENGTH: 1624 base pairs | |
| 201 | | (B) TYPE: nucleic acid | |
| 202 | | (C) STRANDEDNESS: single | |
| 202 | | (D) TOPOLOGY: linear | |
| 203 | | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19: | |
| 204 | | CCGACTGAGG CACGAGCGGG TGACGCTGGG CCTGCAGCGC | 40 |
| | | GGAGCAGAAA GCAGAACCCG CAGAGTCCTC CCTGCTGCTG | 80 |
| 206 | | | 120 |
| 207 | | IGIGGACGAC ACGIGGGCAC AGGCAGAAGI GGGCCCIGIG | |

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| 208 | ACCAGCTGCA CTGGTTTCGT GGAAGGAAGC TCCAGGACTG | 160 |
|-----|---|------|
| 209 | GCGGGATGGG CTCAGCCTGT ATCAAAGTCA CCAAATACTT | 200 |
| 210 | TCTCTTCCTC TTCAACTTGA TCTTCTTTAT CCTGGGCGCA | 240 |
| 211 | GTGATCCTGG GCTTCGGGGT GTGGATCCTG GCCGACAAGA | 280 |
| 212 | GCAGTTTCAT CTCTGTCCTG CAAACCTCCT CCAGCTCGCT | 320 |
| 213 | TAGGATGGGG GCCTATGTCT TCATCGGCGT GGGGGCAGTC | 360 |
| 214 | ACTATGCTCA TGGGCTTCCT GGGCTGCATC GGCGCCGTCA | 400 |
| 215 | ACGAGGTCCG CTGCCTGCTG GGGCTGTACT TTGCTTTCCT | 440 |
| 216 | GCTCCTGATC CTCATTGCCC AGGTGACGGC CGGGGCCCTC | 480 |
| 217 | TTCTACTTCA ACATGGGCAA GCTGAAGCAG GAGATGGGCG | 520 |
| 218 | GCATCGTGAC TGAGCTCATT CGAGACTACA ACAGCAGTCG | 560 |
| 219 | CGAGGACAGC CTGCAGGATG CCTGGGACTA CGTGCAGGCT | 600 |
| 220 | CAGGTGAAGT GCTGCGGCTG GGTCAGCTTC TACAACTGGA | 640 |
| 221 | CAGACAACGC TGAGCTCATG AATCGCCCTG AGGTCACCTA | 680 |
| 222 | CCCCTGTTCC TGCGAAGTCA AGGGGGAAGA GGACAACAGC | 720 |
| 223 | CTTTCTGTGA GGAAGGGCTT CTGCGAGGCC CCCGGCAACA | 760 |
| 224 | GGACCCAGAG TGGCAACCAC CCTGAGGACT GGCCTGTGTA | 800 |
| 225 | CCAGGAGGGC TGCATGGAGA AGGTGCAGGC GTGGCTGCAG | 840 |
| 226 | GAGAACCTGG GCATCATCCT CGGCGTGGGC GTGGGTGTGG | 880 |
| 227 | CCATCATCGA GCTCCTGGGG ATGGTCCTGT CCATCTGCTT | 920 |
| 228 | GTGCCGGCAC GTCCATTCCG AAGACTACAG CAAGGTCCCC | 960 |
| 229 | AAGTACTGAG GCAGCTGCTA TCCCCATCTC CCTGCCTGGC | 1000 |
| 230 | CCCCAACCTC AGGGCTCCCA GGGGTCTCCC TGGCTCCCTC | 1040 |
| 231 | CTCCAGGCCT GCCTCCCACT TCACTGCGAA GACCCTCTTG | 1080 |
| 232 | CCCACCCTGA CTGAAAGTAG GGGGCTTTCT GGGGCCTAGC | 1120 |
| 233 | GATCTCTCCT GGCCTATCCG CTGCCAGCCT TGAGCCCTGG | 1160 |
| 234 | CTGTTCTGTG GTTCCTCTGC TCACCGCCCA TCAGGGTTCT | 1200 |
| 235 | CTTATCAACT CAGAGAAAAA TGCTCCCCAC AGCGTCCCTG | 1240 |
| 236 | GCGCAGGTGG GCTGGACTTC TACCTGCCCT CAAGGGTGTG | 1280 |
| 237 | TATATTGTAT AGGGGCAACT GTATGAAAAA TTGGGGAGGA | 1320 |
| 238 | GGGGGCCGGG CGCGGTGCTC ACGCCTGTAA TCCCAGCACT | 1360 |
| 239 | TTGGGAGGCC GAGGCGGGTG GATCACGAGG TCAGGAGATC | 1400 |
| 240 | GAGACCATCC TGGCTAACAT GGTGAAACCC CGTCTCTACT | 1440 |
| 241 | AAAAATACAA AAAAAATTTA GCCGGGCGCG GTGGCGGGCA | 1480 |
| 242 | CCTGTAGTCC CAGCTACTTG GGAGGCTGAG GCAGGAGAAT | 1520 |
| 243 | GGTGTGAACC CGGGAGCGGA GGTTGCAGTG AGCTGAGATC | 1560 |
| 244 | GTGCTACTGC ACTCCAGCCT GGGGGACAGA AAGAGACTCC | 1600 |
| 245 | GTCTCAAAAA AAAAAAAAA AAAA | 1624 |
| | (2) INFORMATION FOR SEQ ID NO: 20: | |
| 248 | (i) SEQUENCE CHARACTERISTICS: | |
| 249 | (A) LENGTH: 267 amino acids | |
| 250 | (B) TYPE: amino acid | |
| 251 | (C) STRANDEDNESS: unknown | |
| 252 | (D) TOPOLOGY: unknown | |
| 253 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20: | |
| 254 | Met Gly Ser Ala Cys Ile Lys Val Thr Lys Tyr Phe | |
| 255 | 1 5 10 | |
| 256 | Leu Phe Leu Phe Asn Leu Ile Phe Phe Ile Leu Gly | |
| 257 | 15 20 | |
| 231 | 20 | |

VERIFICATION SUMMARY

DATE: 07/26/2005

PATENT APPLICATION: US/10/627,952

TIME: 09:49:43

Input Set : N:\Crf3\RULE60\10627952.raw
Output Set: N:\CRF4\07262005\J627952.raw

L:21 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:22 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:26 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)